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www.elsevier.com/locate/yjtbi

PII: S0022-5193(16)30318-6
DOI: http://dx.doi.org/10.1016/j.jtbi.2016.09.022
Reference: YJTBI8830

To appear in: *Journal of Theoretical Biology*

Received date: 21 April 2016
Revised date: 14 September 2016
Accepted date: 25 September 2016

Cite this article as: Kelvin J. Richards, Viral infections of oceanic plankton blooms, *Journal of Theoretical Biology* http://dx.doi.org/10.1016/j.jtbi.2016.09.022

Viral infections of oceanic plankton blooms

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Abstract

Viruses are known to impact blooms of phytoplankton in the ocean, in some cases causing the bloom to crash. Here, using a population model that includes viral infection, we investigate the conditions under which the presence of a virus significantly impacts the population dynamics. A major focus is how spatial variability influences the spread of an epidemic in a stirring and mixing field. The combination of viral infection and diffusion can cause waves of the epidemic to sweep through the domain, with the epidemic lasting much longer than in the homogeneous case. Stirring by the fluid flow can greatly increase this effect causing an increase in the fraction of the bloom that is affected and in certain circumstances (high diffusion and stirring) can totally suppress the bloom. The fluid environment affects the relative spatial structure of the components of the system. High values of the concentrations of the virus and infected phytoplankton are found in thin filaments along fronts of uninfected (susceptible) phytoplankton.

Keywords: Population dynamics, Stirring and mixing, Spatial structure
PACS: 87.23.Cc, 82.40.Ck, 47.52.+j

1. Introduction

Blooms of phytoplankton occur in the spring in many parts of the ocean, resulting in high concentrations of algal cells. The bloom can be a result of high nutrient and increasing light levels (although this is not always the case: see Behrenfeld, 2010). Blooms crash because of reduced nutrient levels or grazing by zooplankton, or a combination of the two. There is an increasing number of documented cases where viral infection also has a major impact on the dynamics of the bloom. Viral–mediated mortality of algal cells can produce significant reductions in cell concentrations (see e.g. Bratbak et al.,

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